



PCT09

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/980,468

DATE: 05/15/2002  
TIME: 13:51:33

Input Set : A:\980468  
Output Set: N:\CRF3\05152002\I980468.raw

pb

4 <110> APPLICANT: BASF Aktiengesellschaft  
7 <120> TITLE OF INVENTION: D6 acetylenase and D6 desaturase from Ceratodon purpureus  
9 <130> FILE REFERENCE: 99 1388  
11 <140> CURRENT APPLICATION NUMBER: US 09/980,468  
12 <141> CURRENT FILING DATE: 2002-12-03  
14 <150> PRIOR APPLICATION NUMBER: 19925718.3  
15 <151> PRIOR FILING DATE: 1999-06-07  
17 <160> NUMBER OF SEQ ID NOS: 28  
19 <170> SOFTWARE: PatentIn Vers. 2.0  
21 <210> SEQ ID NO: 1  
22 <211> LENGTH: 2040  
23 <212> TYPE: DNA  
24 <213> ORGANISM: Ceratodon purpureus  
26 <220> FEATURE:  
27 <221> NAME/KEY: CDS  
28 <222> LOCATION: (176)..(1627)  
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34 oggcacttgtt gggatgggtga aggagtgtatc gatcaggaggt gcaggagctg cattagtttc 120  
36 tcagggtcga tcaggttatt ctgaaaaagg ctgcgtctgt gagcagtttgc caaaa atg 178  
37 Met  
38 1  
40 gcc ctc gtt acc gac ttt ctg aac ttt ctg ggc acg aca tgg agc aag 226  
41 Ala Leu Val Thr Asp Phe Leu Asn Phe Leu Gly Thr Thr Trp Ser Lys  
42 5 10 15  
44 tac agc gtg tac acc cat agc tat gct gga aac tat ggg cct act ttg 274  
45 Tyr Ser Val Tyr Thr His Ser Tyr Ala Gly Asn Tyr Gly Pro Thr Leu  
46 20 25 30  
48 aag cac gcc aaa aag gtt tct gct caa ggt aaa act gcg gga cag aca 322  
49 Lys His Ala Lys Lys Val Ser Ala Gln Gly Lys Thr Ala Gly Gln Thr  
50 35 40 45  
52 ctg aga cag aga tcg gtg cag gac aaa aag cca ggc act tac tct ctg 370  
53 Leu Arg Gln Arg Ser Val Gln Asp Lys Lys Pro Gly Thr Tyr Ser Leu  
54 50 55 60 65  
56 gcc gat gtt gct tct cac gac agg cct gga gac tgc tgg atg atc gtc 418  
57 Ala Asp Val Ala Ser His Asp Arg Pro Gly Asp Cys Trp Met Ile Val  
58 70 75 80  
60 aaa gag aag gtg tat gat att agc cgt ttt gcg gac gac cac cct gga 466  
61 Lys Glu Lys Val Tyr Asp Ile Ser Arg Phe Ala Asp Asp His Pro Gly  
62 85 90 95  
64 ggg acg gta att agc acc tac ttt ggg cgg gat ggc aca gac gtt ttc 514  
65 Gly Thr Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe  
66 100 105 110

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68	gca	aca	ttc	cat	cca	cct	gcc	gca	tgg	aag	caa	ctc	aat	gac	tac	tac	562
69	Ala	Thr	Phe	His	Pro	Pro	Ala	Ala	Trp	Lys	Gln	Leu	Asn	Asp	Tyr	Tyr	
70	115				120							125					
72	att	gga	gac	ctt	gct	agg	gaa	gag	ccc	ctt	gat	gaa	tgg	ctt	aaa	gac	610
73	Ile	Gly	Asp	Leu	Ala	Arg	Glu	Glu	Pro	Leu	Asp	Glu	Leu	Leu	Lys	Asp	
74	130				135						140				145		
76	tac	aga	gat	atg	aga	gcc	gag	ttt	gtt	aga	gaa	ggg	ctt	ttc	aag	agt	658
77	Tyr	Arg	Asp	Met	Arg	Ala	Glu	Phe	Val	Arg	Glu	Gly	Leu	Phe	Lys	Ser	
78						150					155				160		
80	tcc	aag	gcc	tgg	ttc	ctg	ctt	cag	act	ctg	att	aat	gca	gct	ctc	ttt	706
81	Ser	Lys	Ala	Trp	Phe	Leu	Leu	Gln	Thr	Leu	Ile	Asn	Ala	Ala	Leu	Phe	
82						165				170				175			
84	gct	gcg	agc	att	gcg	act	atc	tgt	tac	gac	aag	agt	tac	tgg	gct	att	754
85	Ala	Ala	Ser	Ile	Ala	Thr	Ile	Cys	Tyr	Asp	Lys	Ser	Tyr	Trp	Ala	Ile	
86						180				185				190			
88	gtg	ctg	tca	gcc	agt	ttg	atg	ggt	ctc	ttc	gtc	caa	cag	tgt	gga	tgg	802
89	Val	Leu	Ser	Ala	Ser	Leu	Met	Gly	Leu	Phe	Val	Gln	Gln	Cys	Gly	Trp	
90						195				200				205			
92	ctt	gcc	cat	gat	ttc	ctt	cat	caa	cag	gtc	ttt	gag	aac	cgt	acc	gcg	850
93	Leu	Ala	His	Asp	Phe	Leu	His	Gln	Gln	Val	Phe	Glu	Asn	Arg	Thr	Ala	
94	210				215					220					225		
96	aac	tcc	ttc	ttt	ggc	tat	ttg	ttc	ggc	aat	tgc	gtg	ctt	ggc	ttt	agt	898
97	Asn	Ser	Phe	Phe	Gly	Tyr	Leu	Phe	Gly	Asn	Cys	Val	Leu	Gly	Phe	Ser	
98						230				235				240			
100	gta	tca	tgg	tgg	agg	acg	aag	cac	aac	att	cat	cat	act	gtt	ccg	aat	946
101	Val	Ser	Trp	Trp	Arg	Thr	Lys	His	Asn	Ile	His	His	Thr	Ala	Pro	Asn	
102						245				250				255			
104	gag	tgc	gac	gaa	cag	tac	aca	cct	cta	gac	gaa	gac	att	gtt	act	ctc	994
105	Glu	Cys	Asp	Glu	Gln	Tyr	Thr	Pro	Leu	Asp	Glu	Asp	Ile	Asp	Thr	Leu	
106						260				265				270			
108	ccc	atc	att	gcc	tgg	agc	aag	gaa	att	ttg	gcc	acc	gtt	gag	agc	aag	1042
109	Pro	Ile	Ile	Ala	Trp	Ser	Lys	Glu	Ile	Leu	Ala	Thr	Val	Glu	Ser	Lys	
110						275				280				285			
112	aga	att	ttg	cga	gtg	ctt	caa	tat	cag	cac	tac	atg	att	ctg	cct	cta	1090
113	Arg	Ile	Leu	Arg	Val	Gln	Tyr	Gln	His	Tyr	Met	Ile	Leu	Pro	Leu		
114	290				295					300				305			
116	ttg	tgc	atg	gcc	cgg	tac	agt	tgg	act	ttt	gga	agt	ttg	ctc	ttc	aca	1138
117	Leu	Phe	Met	Ala	Arg	Tyr	Ser	Trp	Thr	Phe	Gly	Ser	Leu	Leu	Phe	Thr	
118						310				315				320			
120	tcc	aat	cct	gat	ttg	agc	acg	acc	aag	gga	ttg	ata	gag	aag	gga	aca	1186
121	Phe	Asn	Pro	Asp	Leu	Ser	Thr	Thr	Lys	Gly	Leu	Ile	Glu	Lys	Gly	Thr	
122						325				330				335			
124	gtt	gct	ttt	cac	tac	gcc	tgg	ttc	agt	tgg	gct	gcg	ttc	cat	att	ttg	1234
125	Val	Ala	Phe	His	Tyr	Ala	Trp	Phe	Ser	Trp	Ala	Ala	Phe	His	Ile	Leu	
126						340				345				350			
128	ccg	ggt	gtc	gct	aag	cct	ttt	gcg	tgg	atg	gta	gca	act	gag	ctt	gtg	1282
129	Pro	Gly	Val	Ala	Lys	Pro	Leu	Ala	Trp	Met	Val	Ala	Thr	Glu	Leu	Val	
130						355				360				365			
132	gcc	ggt	ttg	ttg	ttg	gga	ttc	gtg	ttt	acg	ttg	agt	cac	aat	gga	aag	1330

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133 Ala Gly Leu Leu Leu Gly Phe Val Phe Thr Leu Ser His Asn Gly Lys				
134 370	375	380	385	
136 gag gtt tac aat gaa tcg aag gac ttc gtg aga gcc cag gtt att acc			1378	
137 Glu Val Tyr Asn Glu Ser Lys Asp Phe Val Arg Ala Gln Val Ile Thr				
138	390	395	400	
140 acc cgt aac acc aag cga ggc tgg ttc aac gat tgg ttc act ggg gga			1426	
141 Thr Arg Asn Thr Lys Arg Gly Trp Phe Asn Asp Trp Phe Thr Gly Gly				
142	405	410	415	
144 ctc gac acc cag att gag cat cac ctg ttt cca aca atg ccc agg cac			1474	
145 Leu Asp Thr Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His				
146	420	425	430	
148 aac tac ccc aag atc gca cct cag gtc gag gct ctt tgc aag aag cac			1522	
149 Asn Tyr Pro Lys Ile Ala Pro Gln Val Glu Ala Leu Cys Lys Lys His				
150	435	440	445	
152 ggc ctc gag tac gat aat gtc tcc gtc gtt ggt gcc tct gtc gcg gtt			1570	
153 Gly Leu Glu Tyr Asp Asn Val Ser Val Val Gly Ala Ser Val Ala Val				
154 450	455	460	465	
156 gtg aag gcg ctc aag gaa att gct gat gaa gcg tca att cgg ctt cac			1618	
157 Val Lys Ala Leu Lys Glu Ile Ala Asp Glu Ala Ser Ile Arg Leu His				
158	470	475	480	
160 gct cac taa gaaatcgctcg aactttgact attcattttt ttccgcctggc			1667	
161 Ala His				
163 tacctcaaat gttcgggagc aggtgcttgg cagtgtgttc aaccggagcg cactgaaaat			1727	
165 gtgcagaatc catttccaga aattaccatt cctagctaa tottctttt accaggtcgg			1787	
167 atatatgaaa ctttttgat gcaacaagta gcattcaatt gaagacattt ttcgagatat			1847	
169 aattcgcagt gtttcttattc agcgggcata cgtactagtc catatcgccg gttgccgaga			1907	
171 gtttacatta ttagtggca caacgagtag atctagtta aatttctatt tccgcatgta			1967	
173 atattactct gaatatatac cgttatctat ttccctaaaa aaaaaaaaaa aaaaaaaaaa			2027	
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179 <211> LENGTH: 483				
180 <212> TYPE: PRT				
181 <213> ORGANISM: Ceratodon purpureus				
183 <400> SEQUENCE: 2				
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188 Lys Tyr Ser Val Tyr Thr His Ser Tyr Ala Gly Asn Tyr Gly Pro Thr				
189	20	25	30	
191 Leu Lys His Ala Lys Lys Val Ser Ala Gln Gly Lys Thr Ala Gly Gln				
192	35	40	45	
194 Thr Leu Arg Gln Arg Ser Val Gln Asp Lys Lys Pro Gly Thr Tyr Ser				
195	50	55	60	
197 Leu Ala Asp Val Ala Ser His Asp Arg Pro Gly Asp Cys Trp Met Ile				
198	65	70	75	80
200 Val Lys Glu Lys Val Tyr Asp Ile Ser Arg Phe Ala Asp Asp His Pro				
201	85	90	95	
203 Gly Gly Thr Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val				
204	100	105	110	
206 Phe Ala Thr Phe His Pro Pro Ala Ala Trp Lys Gln Leu Asn Asp Tyr				

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207	115	120	125
209	Tyr Ile Gly Asp Leu Ala Arg Glu Glu Pro Leu Asp Glu Leu Leu Lys		
210	130	135	140
212	Asp Tyr Arg Asp Met Arg Ala Glu Phe Val Arg Glu Gly Leu Phe Lys		
213	145	150	155
215	Ser Ser Lys Ala Trp Phe Leu Leu Gln Thr Leu Ile Asn Ala Ala Leu		160
216	165	170	175
218	Phe Ala Ala Ser Ile Ala Thr Ile Cys Tyr Asp Lys Ser Tyr Trp Ala		
219	180	185	190
221	Ile Val Leu Ser Ala Ser Leu Met Gly Leu Phe Val Gln Gln Cys Gly		
222	195	200	205
224	Trp Leu Ala His Asp Phe Leu His Gln Gln Val Phe Glu Asn Arg Thr		
225	210	215	220
227	Ala Asn Ser Phe Phe Gly Tyr Leu Phe Gly Asn Cys Val Leu Gly Phe		
228	225	230	235
230	240	205	
231	Ser Val Ser Trp Trp Arg Thr Lys His Asn Ile His His Thr Ala Pro		
233	245	250	255
234	Asn Glu Cys Asp Glu Gln Tyr Thr Pro Leu Asp Glu Asp Ile Asp Thr		
236	260	265	270
237	Leu Pro Ile Ile Ala Trp Ser Lys Glu Ile Leu Ala Thr Val Glu Ser		
239	275	280	285
240	Lys Arg Ile Leu Arg Val Leu Gln Tyr Gln His Tyr Met Ile Leu Pro		
242	290	295	300
243	Leu Leu Phe Met Ala Arg Tyr Ser Trp Thr Phe Gly Ser Leu Leu Phe		
245	305	310	315
246	320	325	335
248	Thr Phe Asn Pro Asp Leu Ser Thr Thr Lys Gly Leu Ile Glu Lys Gly		
249	340	345	350
251	Thr Val Ala Phe His Tyr Ala Trp Phe Ser Trp Ala Ala Phe His Ile		
252	355	360	365
254	Leu Pro Gly Val Ala Lys Pro Leu Ala Trp Met Val Ala Thr Glu Leu		
255	370	375	380
257	Val Ala Gly Leu Leu Leu Gly Phe Val Phe Thr Leu Ser His Asn Gly		
258	385	390	395
260	Lys Glu Val Tyr Asn Glu Ser Lys Asp Phe Val Arg Ala Gln Val Ile		400
261	405	410	415
263	Thr Thr Arg Asn Thr Lys Arg Gly Trp Phe Asn Asp Trp Phe Thr Gly		
264	420	425	430
266	Gly Leu Asp Thr Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg		
267	435	440	445
269	His Asn Tyr Pro Lys Ile Ala Pro Gln Val Glu Ala Leu Cys Lys Lys		
270	450	455	460
272	His Gly Leu Glu Tyr Asp Asn Val Ser Val Val Gly Ala Ser Val Ala		
273	465	470	475
275	Val Val Lys Ala Leu Lys Glu Ile Ala Asp Glu Ala Ser Ile Arg Leu		480
278	His Ala His		
279	<210> SEQ ID NO: 3		
280	<211> LENGTH: 1467		
280	<212> TYPE: DNA		

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281 <213> ORGANISM: Ceratodon purpureus  
283 <220> FEATURE:  
284 <221> NAME/KEY: CDS  
285 <222> LOCATION: (10)..(1461)  
287 <400> SEQUENCE: 3  
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290 Met Ala Leu Val Thr Asp Phe Leu Asn Phe Leu Gly Thr Thr  
291 1 5 10  
293 tgg agc aag tac agc gtg tac acc cat agc tat gct gga aac tat ggg 99  
294 Trp Ser Lys Tyr Ser Val Tyr Thr His Ser Tyr Ala Gly Asn Tyr Gly  
295 15 20 25 30  
297 cct act ttg aag cac gcc aaa aag gtt tct gct caa ggt aaa act gcg 147  
298 Pro Thr Leu Lys His Ala Lys Lys Val Ser Ala Gln Gly Lys Thr Ala  
299 35 40 45  
301 gga cag aca ctg aga cag aga tcg gtg cag gac aaa aag cca ggc act 195  
302 Gly Gln Thr Leu Arg Gln Arg Ser Val Gln Asp Lys Lys Pro Gly Thr  
303 50 55 60  
305 tac tct ctg gcc gat gtt gct tct cac gac agg cct gga gac tgc tgg 243  
306 Tyr Ser Leu Ala Asp Val Ala Ser His Asp Arg Pro Gly Asp Cys Trp  
307 65 70 75  
309 atg atc gtc aaa gag aag gtg tat gat att agc cgt ttt gcg gac gac 291  
310 Met Ile Val Lys Glu Lys Val Tyr Asp Ile Ser Arg Phe Ala Asp Asp  
311 80 85 90  
313 cac cct gga ggg acg gta att agc acc tac ttt ggg cgg gat ggc aca 339  
314 His Pro Gly Gly Thr Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr  
315 95 100 105 110  
317 gac gtt ttc gca aca ttc cat cca cct gcc gca tgg aag caa ctc aat 387  
318 Asp Val Phe Ala Thr Phe His Pro Pro Ala Ala Trp Lys Gln Leu Asn  
319 115 120 125  
321 gac tac tac att gga gac ctt gct agg gaa gag ccc ctt gat gaa ttg 435  
322 Asp Tyr Tyr Ile Gly Asp Leu Ala Arg Glu Glu Pro Leu Asp Glu Leu  
323 130 135 140  
325 ctt aaa gac tac aga gat atg aga gcc gag ttt gtt aga gaa ggg ctt 483  
326 Leu Lys Asp Tyr Arg Asp Met Arg Ala Glu Phe Val Arg Glu Gly Leu  
327 145 150 155  
329 ttc aag agt tcc aag gcc tgg ttc ctg ctt cag act ctg att aat gca 531  
330 Phe Lys Ser Ser Lys Ala Trp Phe Leu Leu Gln Thr Leu Ile Asn Ala  
331 160 165 170  
333 gct ctc ttt gct gcg agc att gcg act atc tgt tac gac aag agt tac 579  
334 Ala Leu Phe Ala Ala Ser Ile Ala Thr Ile Cys Tyr Asp Lys Ser Tyr  
335 175 180 185 190  
337 tgg gct att gtg ctg tca gcc agt ttg atg ggt ctc ttc gtc caa cag 627  
338 Trp Ala Ile Val Leu Ser Ala Ser Leu Met Gly Leu Phe Val Gln Gln  
339 195 200 205  
341 tgt gga tgg ctt gcc cat gat ttc ctt cat caa cag gtc ttt gag aac 675  
342 Cys Gly Trp Leu Ala His Asp Phe Leu His Gln Gln Val Phe Glu Asn  
343 210 215 220  
345 cgt acc gcg aac tcc ttc ttt ggc tat ttg ttc ggc aat tgc gtg ctt 723  
346 Arg Thr Ala Asn Ser Phe Phe Gly Tyr Leu Phe Gly Asn Cys Val Leu

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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:14; N Pos. 3,12,15  
Seq#:15; N Pos. 3,6,12